



#9/43

SEQUENCE LISTING

<110> Bander, Neil H.

<120> TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

<130> Lois M. Kwasigroch: BZL 242/024

<140> US 09/357,704

<141> 1999-07-20

<150> US 08/838,682

<151> 1997-04-09

<150> US 60/016,976

<151> 1996-05-06

<150> US 60/022,125

<151> 1996-07-18

<160> 21

<170> PatentIn version 3.0

<210> 1

<211> 391

<212> DNA

<213> Mus sp.

<400> 1

tctcctgtca ggaactgcag gtgtcctctc tgaggtccag ctgcaacagt ctggacctga 60
actggtgaag cctgggactt cagtgaggat atcctgcaag acttctggat acacattcac 120
tgaatatacc atacactggg tgaagcagag ccatggaaag agccttgagt ggattggaaa 180
catcaatcct aacaatgggtg gtaccaccta caatcagaag ttcgaggaca aggccacatt 240
gactgtagac aagtcctcca gtacagccta catggagctc cgcagcctaa catctgagga 300
ttctgcagtc tattattgtg cagctggttg gaactttgac tactggggcc aaggcaccac 360
tctcacagtc tctcagcca aaacgacacc c 391

<210> 2

<211> 391

<212> DNA

<213> Mus sp.

<400> 2

gggtgtcggt ttggctgagg agactgtgag agtgggtgcct tggccccagt agtcaaagtt 60
ccaaccagct gcacaataat agactgcaga atcctcagat gttaggctgc ggagctccat 120
gtaggctgta ctggaggact tgtctacagt caatgtggcc ttgtcctcga acttctgatt 180
gtagggtgga ccaccattgt taggattgat gtttccaate cactcaaggc tctttccatg 240
gctctgcttc acccagtgtg tggtatattc agtgaatgtg tatccagaag tcttgagga 300

47

T0470

tatcctcact gaagtcaccag gcttcaccag ttcaggtcca gactgttgca gctggacctc 360
agagaggaca cctgcagttc ctagcaggag a 391

<210> 3
<211> 123
<212> PRT
<213> Mus sp.

<400> 3

Ser	Pro	Val	Arg	Asn	Cys	Arg	Cys	Pro	Leu	Gly	Pro	Ala	Ala	Thr	Val
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Trp	Thr	Thr	Gly	Glu	Ala	Trp	Asp	Phe	Ser	Glu	Asp	Ile	Leu	Gln	Asp
			20					25					30		
Phe	Trp	Ile	His	Ile	His	Ile	Tyr	His	Thr	Leu	Gly	Glu	Ala	Glu	Pro
		35					40					45			
Trp	Lys	Glu	Pro	Val	Asp	Trp	Lys	His	Gln	Ser	Gln	Trp	Trp	Tyr	His
	50					55					60				
Leu	Gln	Ser	Glu	Val	Arg	Gly	Gln	Gly	His	Ile	Asp	Cys	Arg	Gln	Val
65					70					75					80
Leu	Gln	Tyr	Ser	Leu	His	Gly	Ala	Pro	Gln	Pro	Asn	Ile	Gly	Phe	Cys
				85					90					95	
Ser	Leu	Leu	Leu	Cys	Ser	Trp	Leu	Glu	Leu	Leu	Leu	Gly	Pro	Arg	His
			100					105					110		
His	Ser	His	Ser	Leu	Leu	Ser	Gln	Asn	Asp	Thr					
		115					120								

<210> 4
<211> 130
<212> PRT
<213> Mus sp.

<400> 4

Leu	Leu	Ser	Gly	Thr	Ala	Gly	Val	Leu	Ser	Glu	Val	Gln	Leu	Gln	Gln
1				5					10					15	
Ser	Gly	Pro	Glu	Leu	Val	Lys	Pro	Gly	Thr	Ser	Val	Arg	Ile	Ser	Cys
			20					25					30		
Lys	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Glu	Tyr	Thr	Ile	His	Trp	Val	Lys
			35				40					45			
Gln	Ser	His	Gly	Lys	Ser	Leu	Glu	Trp	Ile	Gly	Asn	Ile	Asn	Pro	Asn
			50			55					60				
Asn	Gly	Gly	Thr	Thr	Tyr	Asn	Gln	Lys	Phe	Glu	Asp	Lys	Ala	Thr	Leu
65					70					75					80
Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Arg	Ser	Leu
				85					90					95	

Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Ala Gly Trp Asn Phe
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr
115 120 125

Thr Pro
130

<210> 5
<211> 125
<212> PRT
<213> Mus sp.

<400> 5

Leu Ser Cys Gln Glu Leu Gln Val Ser Ser Leu Arg Ser Ser Cys Asn
1 5 10 15

Ser Leu Asp Leu Asn Trp Ser Leu Gly Leu Gln Gly Tyr Pro Ala Arg
20 25 30

Leu Leu Asp Thr His Ser Leu Asn Ile Pro Tyr Thr Gly Ser Arg Ala
35 40 45

Met Glu Arg Ala Leu Ser Gly Leu Glu Thr Ser Ile Leu Thr Met Val
50 55 60

Val Pro Pro Thr Ile Arg Ser Ser Arg Thr Arg Pro His Leu Thr Ser
65 70 75 80

Pro Pro Val Gln Pro Thr Trp Ser Ser Ala Ala His Leu Arg Ile Leu
85 90 95

Gln Ser Ile Ile Val Gln Leu Val Gly Thr Leu Thr Thr Gly Ala Lys
100 105 110

Ala Pro Leu Ser Gln Pro Ser Gln Pro Lys Arg His Pro
115 120 125

<210> 6
<211> 345
<212> DNA
<213> Mus sp.

<400> 6

gaggtccagc tgcaacagtc tggacctgaa ctggtgaagc ctgggacttc agtgaggata 60
tcctgcaaga cttctggata cacattcact gaatatacca tacactgggt gaagcagagc 120
catggaaaga gcottgagtg gattggaaac atcaatccta acaatggtgg taccacctac 180
aatcagaagt tcgaggacaa ggccacattg actgtagaca agtcctccag tacagcctac 240
atggagctcc gcagcctaac atctgaggat tctgcagtct attattgtgc agctgggttg 300
aactttgact actggggcca aggcaccact ctcacagtct cctca 345

<210> 7
<211> 345

<212> DNA
<213> Mus sp.

<400> 7
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ataatagact gcagaatcct cagatgttag gctgcggagc tccatgtagg ctgtactgga 120
ggacttgtct acagtcaatg tggccttgtc ctcgaacttc tgattgtagg tggtaccacc 180
attgttagga ttgatgtttc caatccactc aaggctcttt ccatggctct gcttcaccca 240
gtgtatggta tattcagtga atgtgtatcc agaagtcttg caggatatcc tcaactgaagt 300
cccaggcttc accagttcag gtccagactg ttgcagctgg acctc 345

<210> 8
<211> 115
<212> PRT
<213> Mus sp.

<400> 8
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Thr
1 5 10 15
Ser Val Arg Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr
20 25 30
Thr Ile His Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45
Gly Asn Ile Asn Pro Asn Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe
50 55 60
Glu Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Ala Gly Trp Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr
100 105 110
Val Ser Ser
115

<210> 9
<211> 363
<212> DNA
<213> Mus sp.

<400> 9
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gtaggagaga gggtcacctt gacctgcaag gccagtgaga atgtgggttac ttatgtttcc 120
tggtatcaac agaaaccaga gcagtctcct aaactgctga tatacggggc atccaaccgg 180
tacactgggg tccccgatcg cttcacaggc agtggatctg caacagattt cactctgacc 240

atcagcagtg tgcaggctga agaccttgca gattatcact gtggacaggg ttacagctat 300
 ccgtacacgt tcggaggggg gaccaagctg gaaataaaac gggctgatgc tgcaccaact 360
 gta 363

<210> 10
 <211> 363
 <212> DNA
 <213> Mus sp.

<400> 10
 tacagttggt gcagcatcag cccgttttat ttccagcttg gtccccctc cgaacgtgta 60
 cggatagctg taaccctgtc cacagtgata atctgcaagg tcttcagcct gcaçactgct 120
 gatggtcaga gtgaaatctg ttgcagatcc actgcctgtg aagcgatcgg ggaccccagt 180
 gtaccggttg gatgccccgt atatcagcag tttaggagac tgctctgggt tctgttgata 240
 ccaggaaaca taagtaacca cattctcact ggccttgacg gtcaaggtga ccctctctcc 300
 tactgacatg gacatggatt tgggagattg ggtcattaca atgttcccat cagctccata 360
 taa 363

<210> 11
 <211> 121
 <212> PRT
 <213> Mus sp.

<400> 11

Leu	Tyr	Gly	Ala	Asp	Gly	Asn	Ile	Val	Met	Thr	Gln	Ser	Pro	Lys	Ser
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Met	Ser	Met	Ser	Val	Gly	Glu	Arg	Val	Thr	Leu	Thr	Cys	Lys	Ala	Ser
			20					25					30		
Glu	Asn	Val	Val	Thr	Tyr	Val	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Glu	Gln
		35					40					45			
Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Gly	Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val
	50					55					60				
Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Ala	Thr	Asp	Phe	Thr	Leu	Thr
65					70					75				80	
Ile	Ser	Ser	Val	Gln	Ala	Glu	Asp	Leu	Ala	Asp	Tyr	His	Cys	Gly	Gln
			85					90						95	
Gly	Tyr	Ser	Tyr	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile
		100						105					110		
Lys	Arg	Ala	Asp	Ala	Ala	Pro	Thr	Val							
		115						120							

<210> 12

<211> 114
<212> PRT
<213> Mus sp.

<400> 12

Tyr Met Glu Leu Met Gly Thr Leu Pro Asn Leu Pro Asn Pro Cys Pro
1 5 10 15
Cys Gln Glu Arg Gly Ser Pro Pro Ala Arg Pro Val Arg Met Trp Leu
20 25 30
Leu Met Phe Pro Gly Ile Asn Arg Asn Gln Ser Ser Leu Leu Asn Cys
35 40 45
Tyr Thr Gly His Pro Thr Gly Thr Leu Gly Ser Pro Ile Ala Ser Gln
50 55 60
Ala Val Asp Leu Gln Gln Ile Ser Leu Pro Ser Ala Val Cys Arg Leu
65 70 75 80
Lys Thr Leu Gln Ile Ile Thr Val Asp Arg Val Thr Ala Ile Arg Thr
85 90 95
Arg Ser Glu Gly Gly Pro Ser Trp Lys Asn Gly Leu Met Leu His Gln
100 105 110

Leu Tyr

<210> 13
<211> 116
<212> PRT
<213> Mus sp.

<400> 13

Ile Ile Trp Ser Trp Glu His Cys Asn Asp Pro Ile Ser Gln Ile His
1 5 10 15
Val His Val Ser Arg Arg Glu Gly His Leu Asp Leu Gln Gly Gln Glu
20 25 30
Cys Gly Tyr Leu Cys Phe Leu Val Ser Thr Glu Thr Arg Ala Val Ser
35 40 45
Thr Ala Asp Ile Arg Gly Ile Gln Pro Val His Trp Gly Pro Arg Ser
50 55 60
Leu His Arg Gln Trp Ile Cys Asn Arg Phe His Ser Asp His Gln Gln
65 70 75 80
Cys Ala Gly Arg Pro Cys Arg Leu Ser Leu Trp Thr Gly Leu Gln Leu
85 90 95
Ser Val His Val Arg Arg Gly Asp Gln Ala Gly Asn Lys Thr Gly Cys
100 105 110
Cys Thr Asn Cys
115

<210> 14
 <211> 321
 <212> DNA
 <213> Mus sp.

<400> 14
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 ttgacctgca aggccagtga gaatgtgggtt acttatgttt cctggatatca acagaaacca 120
 gagcagtctc ctaaactgct gatatacggg gcatccaacc ggtacactgg ggtccccgat 180
 cgcttcacag gcagtggatc tgcaacagat ttcactctga ccatcagcag tgtgcaggct 240
 gaagaccttg cagattatca ctgtggacag ggttacagct atccgtacac gttcggaggg 300
 gggaccaagc tggaaataaa a 321

<210> 15
 <211> 321
 <212> DNA
 <213> Mus sp.

<400> 15
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 gtgataatct gcaagggtctt cagcctgcac actgctgatg gtcagagtga aatctgttgc 120
 agatccactg cctgtgaagc gatcggggac cccagtgtac cggttggatg ccccgatatat 180
 cagcagttta ggagactgct ctggtttctg ttgataccag gaaacataag taaccacatt 240
 ctcaactggcc ttgcagggtca aggtgaccct ctctcctact gacatggaca tggatttggg 300
 agattgggtc attacaatgt t 321

<210> 16
 <211> 107
 <212> PRT
 <213> Mus sp.

<400> 16

Asn	Ile	Val	Met	Thr	Gln	Ser	Pro	Lys	Ser	Met	Ser	Met	Ser	Val	Gly
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Glu	Arg	Val	Thr	Leu	Thr	Cys	Lys	Ala	Ser	Glu	Asn	Val	Val	Thr	Tyr
			20					25					30		
Val	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Glu	Gln	Ser	Pro	Lys	Leu	Leu	Ile
		35					40					45			
Tyr	Gly	Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly
	50					55				60					
Ser	Gly	Ser	Ala	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Val	Gln	Ala
65					70					75				80	
Glu	Asp	Leu	Ala	Asp	Tyr	His	Cys	Gly	Gln	Gly	Tyr	Ser	Tyr	Pro	Tyr

53

85

90

95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 17
<211> 321
<212> DNA
<213> Mus sp.

<400> 17
gacattgtga tgaccagtc tcacaaattc atgtccacat cagtaggaga cagggtcagc 60
atcatctgta aggccagtca agatgtgggt actgctgtag actggtatca acagaaacca 120
ggacaatctc ctaaactact gatttattgg gcatccactc ggcacactgg agtccctgat 180
cgcttcacag gcagtggatc tgggacagac ttcactctca ccattactaa tgttcagtct 240
gaagacttgg cagattattt ctgtcagcaa tataacagct atcctctcac gttcgggtgct 300
gggaccatgc tggacctgaa a 321

<210> 18
<211> 321
<212> DNA
<213> Mus sp.

<400> 18
tttcagggtcc agcatgggtcc cagcaccgaa cgtgagagga tagctgttat attgctgaca 60
gaaataatct gccaaagtctt cagactgaac attagtaatg gtgagagtga agtctgtccc 120
agatccactg cctgtgaagc gatcagggac tccagtgtgc cgagtggatg cccaataaat 180
cagtagttta ggagattgtc ctggtttctg ttgataccag tctacagcag taccacatc 240
ttgactggcc ttacagatga tgctgaccct gtctcctact gatgtggaca tgaatttgtg 300
agactgggtc atcacaatgt c 321

<210> 19
<211> 107
<212> PRT
<213> Mus sp.

<400> 19

Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Ser Ile Ile Cys Lys Ala Ser Gln Asp Val Gly Thr Ala
20 25 30

Val Asp Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser
65 70 75 80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Ala Gly Thr Met Leu Asp Leu Lys
100 105

<210> 20
<211> 125
<212> PRT
<213> Mus sp.

<400> 20

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Asn Trp Val Lys Gln Ser Pro Gly Lys Ser Leu Glu Trp
35 40 45

Ile Gly Asp Ile Asn Pro Gly Asn Gly Gly Thr Ser Tyr Asn Gln Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Gly Tyr Tyr Ser Ser Ser Tyr Met Ala Tyr Tyr Ala Phe
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 21
<211> 109
<212> PRT
<213> Mus sp.

<400> 21

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Asp Ile Ser Asn
20 25 30

Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ser Pro Lys Leu Leu
35 40 45

Ile Tyr Tyr Ala Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu

55

65

70

75

80

Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
85 90 95

Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105